

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:23 : Search time 299.73 Seconds  
(without alignments)  
16.815 Million cell updates/sec

Title: US-09-331-631a-5\_COPY\_33\_75

Perfect score: 248  
Sequence: 1 NOEDPQTECCQCRRCROE.....RQOQYCORCKEICEEEY 43

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

```

1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_ricent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	100.0	625	10 Q9SP13	Q9SP13 macadamia i
2	241	97.2	666	10 Q9SP15	Q9SP15 macadamia i
3	235	94.8	666	10 Q9SP14	Q9SP14 macadamia i
4	112	45.2	593	10 Q9SEW4	Q9sew4 juglans reg
5	110	44.4	525	10 Q43358	Q43358 theobroma c
6	96	38.7	411	5 P91419	P91419 caenorhabdi
7	78.5	31.7	425	5 Q17400	Q17400 caenorhabdi
8	78.5	31.7	600	5 Q19594	Q19594 caenorhabdi
9	77	31.0	572	5 Q19594	Q19594 caenorhabdi
10	77	31.0	1513	5 Q19790	Q19790 caenorhabdi
11	75.5	30.4	242	5 Q19919	Q19919 caenorhabdi
12	75	30.2	388	5 Q16500	Q16500 caenorhabdi
13	75	30.2	388	5 Q16501	Q16501 caenorhabdi
14	75	30.2	388	5 Q16501	Q16501 caenorhabdi
15	74	29.8	438	5 Q44606	Q44606 caenorhabdi
16	74	29.8	438	5 Q16502	Q16502 caenorhabdi
17	73.5	29.6	810	10 Q9ZW13	Q9ZW13 cucurbita m
18	73	29.4	330	5 Q18118	Q18118 caenorhabdi
19	73	29.4	339	5 Q9N4R1	Q9N4R1 caenorhabdi

20	72.5	29.2	335	5 Q9N613	Q9N613 caenorha
21	72.5	29.2	393	10 Q9TP0	Q9TP0 oryza sa
22	72	29.0	709	5 Q9N4R2	Q9N4R2 caenorhabdi
23	71.5	28.8	335	5 Q9NE70	Q9NE70 caenorhabdi
24	71.5	28.8	335	5 Q9NE69	Q9NE69 caenorhabdi
25	71.5	28.8	419	5 Q9NA38	Q9NA38 caenorhabdi
26	71.5	28.8	420	5 Q9NA61	Q9NA61 caenorhabdi
27	71	28.6	378	5 Q27383	Q27383 caenorhabdi
28	68.5	27.6	356	5 Q17316	Q17316 ceratilis c
29	67.5	27.2	273	5 Q23390	Q23390 caenorhabdi
30	66.5	26.8	273	5 Q45362	Q45362 caenorhabdi
31	66.5	26.8	637	10 Q03678	Q03678 hordeum vul
32	66.5	26.8	654	5 Q17982	Q17982 caenorhabdi
33	66	26.6	111	5 Q19054	Q19054 caenorhabdi
34	66	26.6	552	5 Q9V152	Q9V152 drosophila
35	65	26.2	539	4 Q9N0A2	Q9N0A2 homo sapien
36	65	26.2	594	5 Q77337	Q77337 plasmodium
37	65	26.2	910	11 Q54899	Q54899 mus musculu
38	65	26.2	910	11 Q86704	Q86704 mus musculu
39	65	26.2	1306	5 Q9TXB8	Q9TXB8 drosophila
40	64	25.8	648	5 Q9N2M8	Q9N2M8 drosophila
41	64	25.8	1080	5 Q9N2M8	Q9N2M8 drosophila
42	63.5	25.6	489	10 Q9SP11	Q9SP11 glycine max
43	63	25.4	243	5 Q9NL90	Q9NL90 entamoeba d
44	63	25.4	1390	5 Q77033	Q77033 dictyostell
45	62	25.0	304	4 Q15409	Q15409 homo sapien

## ALIGNMENTS

RESULT 1					
Q9SP13		PRELIMINARY:	PRT:	625 AA.	
ID Q9SP13					
AC Q9SP13					
DT 01-MAY-2000 (TREMblrel. 13, Created)					
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)					
DT 01-OCT-2000 (TREMblrel. 15, last annotation update)					
DE VICILIN PRECURSOR (FRAGMENT).					
GN AMP2.					
OS Macadamia integrifolia (Macadamia nut).					
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;					
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.					
OX NCBI_Taxid=60698;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=NOT KERNEL;					
RA Marcus J.P., Coulter K.C., Green J.L., Manners J.M.;					
RT "A family of antimicrobial peptides is produced by processing of a 7S					
RT globulin protein in Macadamia integrifolia."					
RL Plant J. 0:0-0(1999).					
DR EMBL: AF161885; AAD54246.1; ..					
DR HSSP: P02853; 2PHL					
DR INTERPRO: IPR001113; ..					
DR PFM: PF00546; Seedstore_7s; 1.					
DR NON_TER					
DR SEQUENCE	625 AA;	73586 MW;	415808A89D370296 CRC64;		

Query Match 100.0%; Score 248; DB 10; Length 625;  
Best Local Similarity 100.0%; Pred. No. 8.3e-22;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NOEDPQTECCQCRRCROESDPROOYTCORCKEICEEEY 43  
|||||  
DB 33 NOEDPQTECCQCRRCROESDPROOYTCORCKEICEEEY 75

RESULT 2  
ID Q9SP15  
AC Q9SP15  
DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE VIOLILIN PRECURSOR.  
GN AMP2.  
OS Macadamia integrifolia (Macadamia nut).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.  
OX NCBI\_TaxID=60698;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=NUT KERNEL;  
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;  
RT "A family of antimicrobial peptides is produced by processing of a 7S  
RT globulin protein in Macadamia integrifolia kernels.";  
RL Plant J. 0:0-0(1999).  
DR EMBL; AF161883; AAD54244.1; -  
DR HSSP; P02853; 2PHT.  
DR INTERPRO: IPR001113; -  
DR PRAM; PF00546; Seedstore\_7s; 1.  
SQ SEQUENCE 666 AA; 78217 MW; C752B884B2DF022A CMC64;

Query Match	97.2%;	Score 241;	DB 10;	Length 666;
Best Local Similarity	97.7%;	Pred. No. 5.9e-21;		
Matches 42;	Conservative	0;	Mismatches 1;	Total 1

QY	1	NOEDPOTECOCORRCROQESDPFOOYTCORCKEICEE	43
db	74	NOEDPOTECOCORRCROESGPRQOYCQRCRKEICEE	116

RESULT	3		
Q9SPL4			
ID	Q9SPL4	PRELIMINARY;	
AC	Q9SPL4;	PRT;	666 AA

DT 01-May-2000 (TREMBLrel. 13, Created)  
DT 01-May-2000 (TREMBLrel. 13, last sequence update)  
DE 01-Oct-2000 (TREMBLrel. 15, last annotation update)  
DE VITILIN PRECURSOR.  
GN AMP2.  
OS *Macademia integrifolia* (Macademia nut).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; Proteaceae; Macademia.  
OX NCBI\_TaxID=60698;  
RN [1]  
RP  
RC  
RC TISSUE=NOT KERNEL;  
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;  
RT "A family of antimicrobial peptides is produced by processing of a 7S  
RL Plant J. 0:0-0(1999)  
DR EMBL: AF161884; AAD54245.1; -  
DR HSSP: P02853; 2PHL.  
DR INTERPRO: IPR001113; -  
DR PFAM: PF00546; Seedstore.7s; 1.  
SO SEQUENCE 666 AA; 78243 MW; 0ECA22F8710F8A7B CRC64;

```

Query Match      94.8%  Score 235;  DB 10;  Length 666
Best Local Similarity 93.0%  2;  Pred. No. 3e-20;
Matches 40;  Conservative 1;  Mismatches 1;  Indels

QY      1  NOEDPOTCCGCGCRRRCROESDPRROOYCCORRCKEICEEERY 43
      74  NODPOTDCCGCGCRRRCROESGPRROOYCCORRCKEICEEERY 116

```

RESULT	4	
09SEW4	ID	09SEW4
09SEW4	PRELIMINARY;	PRT: 593 AA.
09SEW4		
DT	01-MAY-2000	(TREMBlurel, 13, Created)
DT	01-MAY-2000	(TREMBlurel, 13, Last sequence update)

DT 01-OCT-2000 (TREMBLER, 15, Last annotation update)  
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).  
OS Juglans regia (English walnut).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons: core eudicots; Rosidae; eustroids I;  
OC Fagales; Juglandaceae; Juglans.  
OX NCBI\_TaxID=51240;  
RN (1)  
RP  
RC SEQUENCE FROM N.A.  
RA STRAIN=CV\_SUNLAND; TISSUE=SONATIC EMBRYO LINE;  
RA Teuber S.S., Jarvis K.C., Peterson W.R., Danekar A.M., Ansari A.A.;  
RT 'Identification and cloning of a cDNA encoding a vicilin-like protein,  
RT Jug 1.2, from English walnut kernel (Juglans regia): a major food  
RT allergen'.  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF066055; AAF18269.1; -.  
DR HSSP; P02853; 2PHL.  
DR INTERPRO: IPR001113; -.  
DR PFAM: PF00546; Seedstore\_7s; 1.  
FT NON\_TER  
SQ SEQUENCE 593 AA; 69990 MW; 9BA127E1919AC0E C0664

Query Match	45.2%;	Score 112;	DB 10;	Length 593;
Best Local Similarity	48.8%;	Pred. No. 8.4e-06;		
Matches	20;	Conservative 7;	Mismatches 14;	

QY 1 NQEDPQTECGCGRCRCQESDPQQQTCQRKCFCEEE 41  
| | : : : | | | | | | | : : :  
Db 10 NPRDPQRYRQCQCYRRGCGQRQ000CQINCEERLEEDQ 50

RESULT	5	
Q43358		
ID	Q43358	PRELIMINARY;
AC	Q43358;	PRT; 525 AA

OS Theobroma cacao (Cacao).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OC Malvales; Malvaceae; Theobroma.  
ON NCBI-TaxID=3641.  
GN VILCIN PRECURSOR.  
DT 01-NOV-1996 (TREMBLrel\_01, Created)  
DT 01-NOV-1996 (TREMBLrel\_01, last sequence update)  
DT 01-OCT-2000 (TREMBLrel\_15, last annotation update)  
ID VILCIN PRECURSOR.

SEQUENCE FROM N.A.  
TISSUE-LEAVES;  
MEDLINE=92288309; PubMed=1600151;  
McHenry L., Fritz P.J.;  
"Comparison of the structure and nucleotide sequences of vicilin genes  
of cocoa and cotton raise questions about vicilin evolution.";   
Plant Mol. Biol. 18:1173-1176(1992).  
EMBL: X62625; CAA44493.1

DR	HSSP; P02853; 2PH.			
DR	MENDL; 30919; Thecc;1188;30919.			
DR	INTERRO; IPR00113; -			
DR	PFAM; PF00546; seedstore_7s; 1.			
DR	PRODOM; PD081059; -; 1.			
DR	Signal.			
FT	SIGNAL.	1	24	POTENTIAL.
FT	CHAIN	25	525	VICLIN.
SO	SEQUENCE	525 AA;	60798 MW;	19114DCSC248905D CRC64

```

Query Match          44.48;  Score 110;  DB 10;  Length 525;
Best Local Similarity 47.58;  Pred. No. 1.3e-05;
Matches 19;  Conservative 10;  Mismatches 11;  Indels 0;  Gaps 0;

OY  2 QEDPOTECOCOCRCRQOQESDPRQOQYQCRKCEEE 41
    : : : : : : : : : : : : : : : : : : : :

```



DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, last sequence update)  
DI 01-OCT-2000 (TrEMBLrel. 15, last annotation update)  
DE HYPOHETHELICAL 62.4 KDA PROTEIN F19G12.7 IN CHROMOSOME X PRECURSOR.  
GN F19G12.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea  
OC Rhabditiidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_Taxid=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Nhan M., Le T.T.;  
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO FAMILY UPE.  
DR EMBL: U51997; AAC8159.1; -  
DR MORMPep: F19G12.7; CE07090.  
KW Hypoethetical protein; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 572 POTENTIAL.  
SO SEQUENCE 572 AA; 62384 MW; BD45B2FDD850AAB9 CRC64; HYPOHETHELICAL PROTEIN F19G12.7.

Query Match	31.0%;	Score 77;	DB 5;	Length 572;
Best Local Similarity	34.0%;	Pred. No. 0.11;		
Matches 17; Conservative	8;	Mismatches 7;	Indels 18;	Gaps 3
Oy	8	ECQCGCRRCRQ-----	QESPRROQYTCGRCKE---ICEE	40
Db	381	OCQCCQNTCCQCPAPYCEBQGCASLCHQPSAPCCQ--CQNTCCQCFAPCECQ		429

RESULT	10	
ID	017970	
AC	017970	PRELIMINARY; PRT: 1513 AA.
DT	01-JAN-1998 (TrEMBLrel. 05, Created)	
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	
DE	M02G9.1 PROTEIN.	
GN	M02G9.1.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Petaloderinae; Caenorhabditis.	
OX	NCBI_TaxId=6239;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RL	Mathews L.;	
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=94150718; PubMed=7906398;	
RA	Wilson R., Alnsough R., Anderson K., Baynes C., Barks M.,	
RA	Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,	
RA	Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,	
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,	
RA	Jones M., Kershaw J., Kirsten J., Laister N., Latille P.,	
RA	Lightning T., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,	
RA	Parsons J., Percy C., Ritken L., Roopra A., Saunders D., Shownkeen R.,	
RA	Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,	
RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,	
RA	Watson A., Weinstein L., Wilkinson-Sproat J., Wohldman P.;	
RT	2.2 Mb of contiguous nucleotide sequence from chromosome III of C.	
RL	Nature 368:32-38(1994).	
DR	EMBL: Z81573; CAB04625.1; -	
DR	HSP: 046655; ICHJ.	
QO	SEQUENCE 1513 AA; 161578 MW; 10BCB4287BA282B5 CRC64;	

Query Match	31.08;	Score 77;	DB 5;	Length 1513;
Best Local Similarity	43.68;	Pred. NO. 0.24;		
Matches 17; Conservative	2;	Mismatches 16;	Indels 4;	Gaps 2

QY 3 EDPTQECQ-CQNRCKQESDPRQQYQCRKEICEE 40  
| | | | : | | | | |  
Db 1141 EQQCCPQQTCTGCGQHNPDAR--VQGNVCVEVCASE 1170

RESULT	1.1	
ID	019919	
PRELIMINARY;		
PRT;	242	AA

DT 01-JUN-1998 (TEMBLrel. 06, Created)  
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)  
DT 01-JUN-1998 (TEMBLrel. 06, Last annotation update)  
DE HYPOTHETICAL 26.2 KDA PROTEIN F3IA3.1 IN CHROMOSOME X.  
GN F3IA3.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromidorea; Rhabditida; Rhabditicoidea  
OC Rhabditidae; Pelodolerinae; Caenorhabditis.  
OX NCBI\_taxid=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Murray J., Le T.T.;  
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.  
CC 1-1 SIMILARITY: BELONGS TO THE FAMILY UPP.  
DR EMBL: U58742; AAB36856.1; -  
DR MOMP: F3IA3.1; CE07158.  
DR Hypothetical protein. 23 Transmembrane.  
FT TRANSMEM 3 POTENTIAL.  
SQ SEQUENCE 242 AA; 26213 MW; C/D69966B00829317 CRC64;

Query Match	30.48%	Score 75.5;	DB 5;	Length 242;
Best Local Similarity	33.38%	Pred. No. 0.06;		
Matches	17;	Conservative	12;	Mismatches 11;
				Indels 11;
				Gaps 4
QY	2	QEDPDECCGCCRCR-----QESDPR-QOQY---QGRCKELCEEEB	42	
	:	:		
	77	QQPAPACCGCCGANTCCQASAPVCQCCGAPCCQCFAPACQ--CQNSCQQTQO	126	

RESULT	12			
016500				
ID	016500	PRELIMINARY;	PRT;	388 AA.
AC	016500;			
DT	01-JAN-1998 (TEMBRel. 05, Created)			
DT	01-JAN-1998 (TEMBRel. 05, Last sequence update)			
DT	01-NOV-1998 (TEMBRel. 08, Last annotation update)			
DE	CO3A7.4. PROTEIN.			
CN	CO3A7.4.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
FX	MEDLINE=94150718; PubMed=7906398;			
RA	Wilson R., Alnsough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P., Raes M., Kershaw J., Kirsten J., Lalster N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rilken L., Roopa A., Saunders D., Showkneen R., Smailton N., Smith A., Sonnenhammer E., Staden R., Sulston J., Thierley-Mieg J., Thomas K., Vandin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.; RT			
RT	"2.2 Mb of sequencing nucleotide sequence from chromosome III of C. elegans."			
RL	Nature 368:32-38(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			

RC STRAIN-BRISTOL N2;  
RA Greco T., Bradshaw H., Elliott G.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF016451; AAB66001.1; -  
SQ SEQUENCE 388 AA; 42139 MW; 2E20655B099AE92 CRC64;

Query Match 30.2%; Score 75; DB 5; Length 388;  
Best Local Similarity 37.5%; Pred. No. 0.13;  
Matches 15; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

OY 2 QEDPOTEC-QCCORRCQDESPPRO-QQYQRCRKEICEE 39  
DB 194 QACQPCQCCQCCSCCVQDQDQNSNCEPACNCTCSDICQ 233

RESULT 13  
ID 016501 PRELIMINARY; PRT; 388 AA.  
AC 016501;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE C03A7.7 PROTEIN.  
GN C03A7.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditioidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA MEDLINE=94150718; PubMed-7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";  
RT Nature 368:32-38(1994).  
RL [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Greco T., Bradshaw H., Elliott G.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF016451; AAB65996.1; -  
SQ SEQUENCE 388 AA; 42129 MW; 7ACA3953E0AF2A2 CRC64;

Query Match 30.2%; Score 75; DB 5; Length 388;  
Best Local Similarity 37.5%; Pred. No. 0.13;  
Matches 15; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

OY 2 QEDPOTEC-QCCORRCQDESPPRO-QQYQRCRKEICEE 39  
DB 194 QACQPCQCCQCCSCCVQDQDQNSNCEPACNCTCSDICQ 233

RESULT 14  
ID 044606 PRELIMINARY; PRT; 388 AA.  
AC 044606;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE R09B5.5 PROTEIN.  
GN R09B5.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditioidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA MEDLINE=94150718; PubMed-7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";  
RT Nature 368:32-38(1994).  
RL [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Sammons L., Wohlmann P., Bauer C., Antoniou B., Wilson R.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF039046; AAB94214.1; -  
SQ SEQUENCE 388 AA; 41440 MW; EA9C34AA4EABFE46 CRC64;

Query Match 30.2%; Score 75; DB 5; Length 388;  
Best Local Similarity 22.2%; Pred. No. 0.13;  
Matches 14; Conservative 15; Mismatches 12; Indels 22; Gaps 2;

OY 2 QEDPOTEC-QCCORRCQ-----QSDPQQQYQRCRKEICEE 39  
DB 147 QQQPASCQPCQCCQCCNVACDAPATSTQAPQVYHLEIQDQAGQCCQCCQSSCTQ 206

OY 40 EEE 42  
DB 207 QQQ 209

RESULT 15  
ID 016502 PRELIMINARY; PRT; 438 AA.  
AC 016502;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE C03A7.8 PROTEIN.  
GN C03A7.8.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditioidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.

